Molecular characterization of *Plasmodium falciparum* dihydrofolate reductase (dhfr) and dihydropteroate synthase (dhps) mutations in isolates from eastern Sudan

Background

In Sudan sulfadoxine-pyrimethamine (SP) was the second line antimalarial treatment for uncomplicated falciparum malaria till June 2004 when the first and second line antimalarial drugs have been switched to Artesunate plus SP and Artemether plus lumefanterene, respectively. Treatment failure caused by SP resistant *P. falciparum* has been reported in Khartoum, eastern and southern Sudan.

Objectives

This study aimed at providing baseline information on the distribution of *Pfdhfr*, *Pfdhps* SP resistance determinant haplotypes to guide future policies for malaria treatment in Sudan.

Methods

PCR and ELISA based technology was used to examine single nucleotide polymorphisms in *Pfdhfr* and *Pfdhps* genes, known to be associated with SP resistance in pretreatment isolates obtained from New Halfa and Kassala sites, eastern Sudan during the malaria transmission season of 2005.

Results

Quintuple mutant parasite at *Pfdhfr* 51/59/108 and at *Pfdhps* 437/540 was found in New Halfa (2.9%) and in Kassala (5.9%). The frequency of *Pfdhfr* triple mutant haplotype was 2.5% in New Halfa and 4.1% in Kassala. In both sites, *Pfdhps* haplotype harboring (437G/540E) is the most frequent *Pfdhps* mutant haplotype yielding a percentage of 17.7% in New Halfa and 62.5% in Kassala.

Conclusions

In the two study sites effectiveness of SP is expected. Detection of *Pfdhfr* triple, and *Pfdhps* double mutant haplotypes, in addition to the quintuple mutations at *Pfdhfr* and *Pfdhps* key positions; in both sites is disturbing, since SP is a component of the first line antimalarial drug in Sudan.